WHAT IS CLAIMED IS:

1. An oligonucleotide comprising at least 8 to about 100 consecutive bases from the sequence of Figure 1 or Figure 2, or the complement of the sequence, wherein the at least 8 to about 100 consecutive bases includes at least one polymorphic site of Table 1.

2. The oligonucleotide of claim 1, wherein the polymorphic site is at base 61465 of Figure 1.

3. The oligonucleotide of claim 1, wherein the polymorphic site is at base 35983 of Figure 1.

4. An oligonucleotide pair selected from the sequence of Figure 1 or Figure 2 or its complement for amplification of a polymorphic site of Table 1.

5. An isolated nucleic acid molecule comprising about 100 consecutive bases to about 235 KB substantially identical to the sequence of Figure 1 or Figure 2, wherein the DNA molecule comprises at least one polymorphic site of Table 1.

6. The isolated nucleic acid molecule of claim 5, wherein the polymorphic site is at base 61465 of Figure 1.

7. The isolated nucleic acid molecule of claim 5, wherein the polymorphic site is at base 35983 of Figure 1.

8. The isolated nucleic acid molecule of claim 5, wherein the nucleic acid is cDNA.

9. The isolated nucleic acid molecule of claim 5, wherein the nucleic acid is RNA.

10. The isolated nucleic acid molecule of claim 5, wherein the nucleic acid is genomic DNA.

11. The isolated nucleic acid molecule of claim 5, wherein the sequence of the nucleic acid molecule is identical to that of Figure 2.

12. A polypeptide encoded by the nucleic acid molecule of claim 5.

13. An antibody which specifically recognizes the polypeptide of claim 12.

14. A method to determine the presence or absence of the common hereditary hemochromatosis (HH) gene mutation in an individual comprising:

providing DNA or RNA from the individual; and

assessing the DNA or RNA for the presence or absence of a haplotype of Table 1,

wherein, as a result, the absence of a haplotype of Table 1 indicates the likely absence of the HH gene mutation in the genome of the individual and the presence of the haplotype indicates the likely presence of the HH gene mutation in the genome of the individual.

15. The method of claim 14, wherein the method further comprises assessing the RNA or DNA for the presence of 24d1 and/or 24d2.

16. The method of claim 14, wherein the method further comprises assessing the RNA or DNA for the presence of at least one of polymorphisms HHP-1, HHP-19, or HHP-29, or microsatellite repeat alleles 19D9:205; 18B4:235; 1A2:239; 1E4:271; 24E2:245; 2B8:206; 3321-1:98; 4073-1:182; 4440-1:180; 4440-2:139; 731-1:177; 5091-1:148; 3216-1:221; 4072-2:170; 950-1:142; 950-2:164; 950-3:165; 950-4:128; 950-6:151; 950-8:137; 63-1:151; 63-2:113; 63-3:169; 65-1:206; 65-2:159; 68-1:167; 241-5:108; 241-29:113; 373-8:151; and 373-29:113, D6S258:199, D6S265:122, D6S105:124; D6S306:238; D6S464:206; or D6S1001:180.

17. The method of claim 14, wherein the haplotype comprises at least two polymorphic sites of Table 1.

18. The method of claim 17, wherein one of the at least two polymorphic sites of Table 1 is at base 35983 or 61465 of Figure 1.

19. The method of claim 13, wherein the haplotype comprises at least three polymorphic sites of Table 1.

20. A method to determine the presence or absence of the common hereditary hemochromatosis (HH) gene mutation in an individual comprising:

providing DNA or RNA from the individual; and

assessing the DNA or RNA for the presence or absence of a genotype defined by a polymorphic allele of Table 1,

wherein, as a result, the absence of a genotype defined by a polymorphic allele of Table 1 indicates the likely absence of the HH gene mutation in the genome of the individual and the presence of the genotype indicates the likely presence of the HH gene mutation in the genome of the individual.

21. The method of claim 20, wherein the polymorphic allele occurs in less than about 50% of a random population of individuals.

22. The method of claim 20, wherein the polymorphic allele occurs in less than about 25% of a random population of individuals.

23. The method of claim 20, wherein the polymorphic allele occurs in less than about 5% of a random population of individuals.

24. The method of claim 20, wherein the genotype is C182.1G7C.

25. The method of claim 20, wherein the genotype is C195.1H5T.

26. A kit comprising one or more oligonucleotides of claim 1.

27. A kit comprising at least one oligonucleotide pair of claim 4.

28. A culture of lymphoblastoid cells having the designation HC14.